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WHAT IS CLAIMED IS:

1. A composition of mammalian leukemia stem cells, wherein at least 50% of the cells in said composition are said leukemia stem cells (LSC).

- 2. The composition according to Claim 1, wherein at least 75% of the cells in said composition are LSC.
 - 3. The composition according to Claim 1, wherein said LSC are human cells.
- 4. The composition according to Claim 3, wherein said LSC have the cell surface phenotype of a hematopoietic progenitor cell, but have acquired an activated β -catenin pathway.
- 5. The composition according to Claim 4, wherein said cells are Thy-1⁻, IL-7R α (CD127)⁻, and lineage panel⁻.
- 6. The composition of Claim 5, wherein said cells are further characterized as IL-3R α^{lo} CD45RA † .
- 7. The composition of Claim 6, wherein said granulocyte monocyte committed progenitor cells are mouse cells and are further characterized as Fc_γR⁺CD34⁺.
- A method of enrichment for a composition of LSC, the method comprising: combining reagents that specifically recognize Thy-1, IL-7Rα (CD127), and a lineage panel with a sample suspected of comprising LSC; and

selecting for those cells that are Thy-1⁻, IL-7Rα (CD127)⁻, and lineage panel⁻.

- 9. The method according to Claim 8, wherein said sample is a blood sample from a leukemia patient.
- 10. The method according to Claim 9, wherein said leukemia patient is a chronic myelogenous leukemia patient.
- 11. A method for the identification of LSC, the method comprising:
 introducing into a sample of leukemia cells a nucleic acid construct comprising
 sequences encoding a detectable marker, which marker is operably linked to a transcriptional

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response element regulated by β-catenin;

detecting the presence of expression of said detectable marker, wherein expression of said marker is indicative that a cell is an LSC cell.

- 12. The method according to Claim 11, wherein said marker is a fluorescence producing protein.
- 13. The method according to Claim 12, wherein said transcriptional response element regulated by β -catenin is a LEF-1/TCF binding sequence.
- 14. The method according to Claim 13, further comprising the step of selecting for cells expressing said detectable marker.
 - 15. A method of phenotyping a leukemic condition, the method comprising:

combining a hematologic sample from a patient suspected of said leukemic condition with specific binding members that are sufficient to distinguish the distribution of cells with hematopoietic stem and progenitor subsets;

determining the distribution of progenitor cells between said subsets,

wherein the distribution of progenitor cells is indicative of the phenotype of said leukemic condition.

- The method according to Claim 15, wherein said leukemic condition is MDS.
- 17. The method according to Claim 15, wherein said leukemic condition is a myeloid leukemia.
- 18. The method according to Claim 15, wherein said myeloid leukemia is CML or CMML.
- 19. The method according to Claim 15, wherein said hematopoietic stem and progenitor subsets include one or more of HSC, CMP, MEP and GMP.
- 20. The method according to Claim 15, wherein said specific binding members are antibodies.
- 21. The method according to Claim 20, wherein said antibodies include specificities for CD34 and CD38.

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22. The method according to Claim 21, wherein said antibodies further include specificities for IL-3R and CD45RA.

- 23. The method according to Claim 21, further comprising antibodies specific for a lineage panel.
 - 24. A kit for use in any of the methods set forth in Claims 1-23.
- 25. A method of screening a candidate chemotherapeutic agent for effectiveness against an LSC, the method comprising:

contacting said agent with the cell composition of Claim 1, and determining the effectiveness of said agent against said LSC.

- 26. A method of inhibiting the proliferation of an LSC, the method comprising: contacting said LSC with an agent that inhibit the Wnt/β-catenin pathway.
- 27. The method according to Claim 26, wherein said agent comprises axin, a polynucleotide encoding axin and operably linked to a transcriptional regulatory element expressed in said LSC, or a mimetic of axin.